

=> fil reg; d que 13  
FILE 'REGISTRY' ENTERED AT 09:29:58 ON 01 DEC 2004  
USE IS SUBJECT TO THE TERMS OF YOUR STN CUSTOMER AGREEMENT.  
PLEASE SEE "HELP USAGETERMS" FOR DETAILS.  
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Property values tagged with IC are from the ZIC/VINITI data file  
provided by InfoChem.

STRUCTURE FILE UPDATES: 29 NOV 2004 HIGHEST RN 790629-40-2  
DICTIONARY FILE UPDATES: 29 NOV 2004 HIGHEST RN 790629-40-2

TSCA INFORMATION NOW CURRENT THROUGH MAY 21, 2004

Please note that search-term pricing does apply when  
conducting SmartSELECT searches.

Crossover limits have been increased. See HELP CROSSOVER for details.

Experimental and calculated property data are now available. For more  
information enter HELP PROP at an arrow prompt in the file or refer  
to the file summary sheet on the web at:

<http://www.cas.org/ONLINE/DBSS/registryss.html>

L2 35 SEA FILE=REGISTRY ABB=ON GUGGUGUCACAGGAAGAGGUC|GACCUCUUCCUGUGA  
CACCAC|GUGGUGUCACAGGAAGAGGUU|AACCUCCUCCUGUGACACCAC|ACUAUAGGCCAG  
AGAGGCUGC|GCAGCCUCUCUGGCCUAUAGU/SQSN  
L3 6 SEA FILE=REGISTRY ABB=ON L2 AND SQL<101

=> d rn cn kwic nte lc 13 1-6

L3 ANSWER 1 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 758728-95-9 REGISTRY  
CN DNA, d(A-C-T-A-T-A-G-G-C-C-A-G-A-G-G-C-T-G-C) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 3: PN: US20040191822 SEQID: 3 claimed DNA  
SQL 21

SEQ 1 actataggcc agagaggctg c  
===== ===== =

HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS, USPATFULL

L3 ANSWER 2 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 758728-94-8 REGISTRY  
CN DNA, d(G-T-G-G-T-G-T-C-A-C-A-G-G-A-A-G-A-G-G-T-T) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 2: PN: US20040191822 SEQID: 2 claimed DNA  
SQL 21

SEQ 1 gtgggtcgtc acggaaagggt t  
===== ===== =

HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS, USPATFULL

L3 ANSWER 3 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN

RN 758728-93-7 REGISTRY  
CN DNA, d(G-T-G-G-T-G-T-C-A-C-A-G-G-A-A-G-A-G-G-T-C) (9CI) (CA INDEX NAME)  
OTHER NAMES:  
CN 1: PN: US20040191822 SEQID: 1 claimed DNA  
SQL 21

SEQ 1 gtgggtcac aggaagaggt c  
===== ===== =  
HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS, USPATFULL

L3 ANSWER 4 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 503196-89-2 REGISTRY  
CN DNA, d(A-C-T-A-T-A-G-G-C-C-A-G-A-G-A-G-G-C-T-G-C) (9CI) (CA INDEX NAME)  
SQL 21

SEQ 1 actataggcc agagaggctg c  
===== ===== =  
HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS

L3 ANSWER 5 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 503196-88-1 REGISTRY  
CN DNA, d(G-T-G-G-T-G-T-C-A-C-A-G-G-A-A-G-A-G-G-T-T) (9CI) (CA INDEX NAME)  
SQL 21

SEQ 1 gtgggtcac aggaagaggt t  
===== ===== =  
HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS

L3 ANSWER 6 OF 6 REGISTRY COPYRIGHT 2004 ACS on STN  
RN 503196-87-0 REGISTRY  
CN DNA, d(G-T-G-G-T-G-T-C-A-C-A-G-G-A-A-G-A-G-G-T-C) (9CI) (CA INDEX NAME)  
SQL 21

SEQ 1 gtgggtcac aggaagaggt c  
===== ===== =  
HITS AT: 1-21

\*\*RELATED SEQUENCES AVAILABLE WITH SEQLINK\*\*  
LC STN Files: CA, CAPLUS

=> fil capl uspatf; s 13  
FILE 'CAPLUS' ENTERED AT 09:30:27 ON 01 DEC 2004  
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FILE 'USPATFULL' ENTERED AT 09:30:27 ON 01 DEC 2004  
CA INDEXING COPYRIGHT (C) 2004 AMERICAN CHEMICAL SOCIETY (ACS)

L4 3 L3

=> dup rem 14

PROCESSING COMPLETED FOR L4

L5 2 DUP REM L4 (1 DUPLICATE REMOVED)  
ANSWERS '1-2' FROM FILE CAPLUS

=> d ibib ed ab hitrn 1-2; fil hom

L5 ANSWER 1 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN DUPLICATE 1  
ACCESSION NUMBER: 2004:803874 CAPLUS Full-text  
DOCUMENT NUMBER: 141:272607  
TITLE: Real-time polymerase chain reaction-based genotyping assay for single nucleotide polymorphism on human gene MDR1 and CYP3A5  
INVENTOR(S): Yates, Charles R.; Miller, Duane; Gourley, Dick; Song, Pengfei  
PATENT ASSIGNEE(S): USA  
SOURCE: U.S. Pat. Appl. Publ., 16 pp.  
CODEN: USXXCO  
DOCUMENT TYPE: Patent  
LANGUAGE: English.  
FAMILY ACC. NUM. COUNT: 1  
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 2004191822	A1	20040930	US 2004-809757	20040325
WO 2004092399	A2	20041028	WO 2004-US9078	20040325
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW				
RW: BW, GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PL, PT, RO, SE, SI, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				

PRIORITY APPLN. INFO.: US 2003-457512P P 20030325

ED Entered STN: 01 Oct 2004

AB The present invention provides fluorescence-based real-time PCR assays for the rapid detection of single nucleotide polymorphisms (SNPs). The genotyping assay can be used to detect SNPs of a number of genes of interest that include, but are not limited to, the human multidrug resistance gene (MDR1) single nucleotide polymorphisms C3435T and G2677T, and cytochrome P 450 3A5 single nucleotide polymorphisms CYP3A5\*3 (A22893G) and CYP3A5\*6 (G30597A).

IT 758728-93-7 758728-94-8 758728-95-9

RL: ARG (Analytical reagent use); DGN (Diagnostic use); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(primer sequence; real-time polymerase chain reaction-based genotyping assay for single nucleotide polymorphism on human gene MDR1 and CYP3A5)

L5 ANSWER 2 OF 2 CAPLUS COPYRIGHT 2004 ACS on STN  
ACCESSION NUMBER: 2002:959448 CAPLUS Full-text  
DOCUMENT NUMBER: 138:266175  
TITLE: Detection of MDR1 single nucleotide polymorphisms C3435T and G2677T using real-time polymerase chain reaction: MDR1 single nucleotide polymorphism genotyping assay  
AUTHOR(S): Song, Pengfei; Li, Shen; Meibohm, Bernd; Gaber, A. Osama; Honaker, Marsha R.; Kotb, Malak; Yates, Charles R.  
CORPORATE SOURCE: Department of Pharmaceutical Sciences, University of Tennessee, Memphis, TN, 38163, USA

SOURCE: PharmSci [online computer file] (2002), 4(4), No pp. given  
given  
CODEN: PHARFY; ISSN: 1522-1059  
URL: <http://www.pharmsci.org/scientificjournals/pharmsci/journal/pdf/ps040429.pdf>

PUBLISHER: American Association of Pharmaceutical Scientists  
DOCUMENT TYPE: Journal; (online computer file)  
LANGUAGE: English

ED    Entered STN: 19 Dec 2002

AB    The objective of this study was to develop a real-time polymerase chain reaction (PCR) method to detect MDR1 (human multidrug resistance gene) single nucleotide polymorphisms (SNPs) C3435T and G2677T. C3435T and G2677T are linked to MDR1\*2, which is associated with enhanced efflux activity in vitro. Using the Smart Cycler, an allele-specific real-time PCR-based genotyping method was developed to detect C3435T and G2677T. The MDR1 genotype of human genomic DNA templates was determined by direct DNA sequencing. PCR reactions for genotyping C3435T and G2677T by using allele-specific primers were conducted in sep. tubes. An addnl. nucleotide mismatch at the third position from the 3' end of each allele-specific primer was used to abrogate nonspecific PCR amplification. The fluorescence emitted by SYBR Green I was monitored to detect formation of specific PCR products. PCR growth curves exceeding the threshold cycle were considered pos. Fluorescence melt-curve anal. was used to corroborate results from PCR growth curves. Using PCR growth curves, our assay accurately determined hetero- and homozygosity for C3435T and G2677T. Genotype assignments based on PCR growth curve, melt-curve anal., agarose gel electrophoresis, and direct DNA sequencing results of PCR products were in perfect agreement. We have developed a rapid MDR1 genotyping method that can be used to assess the contribution of MDR1\*2 to pharmacokinetic and pharmacodynamic variability of P-glycoprotein substrates.

IT    503196-87-0 503196-88-1 503196-89-2

RL: ARG (Analytical reagent use); BUU (Biological use, unclassified); PRP (Properties); ANST (Analytical study); BIOL (Biological study); USES (Uses)  
(SNP C3435T-specific primer; use of allele-specific real-time PCR for detection of single nucleotide polymorphisms (SNPs) C3435T and G2677T present in human MDR1 gene, wherein said SNPs are associated with aberrant allele MDR1\*2)

REFERENCE COUNT:                    23                    THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

FILE 'HOME' ENTERED AT 09:30:40 ON 01 DEC 2004

=>

Run on: November 30, 2004, 16:28:09 ; Search time 727.333 Seconds  
(without alignments)  
1365.376 Million cell updates/sec

Title: SEQ1  
Perfect score: 21  
Sequence: 1 gtgggtcacaggaagaggc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenEmbl:  
1: gb\_ba:  
2: gb\_htg:  
3: gb\_in:  
4: gb\_om:  
5: gb\_ov:  
6: gb\_pat:  
7: gb\_ph:  
8: gb\_pl:  
9: gb\_pr:  
10: gb\_ro:  
11: gb\_sts:  
12: gb\_sy:  
13: gb\_un:  
14: gb\_vi:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query				Description
	Score	Match	Length	DB ID	
<hr/>					
1	19.4	92.4	247	6 AX706977	AX706977 Sequence
2	19.4	92.4	247	6 AX707907	AX707907 Sequence
3	19.4	92.4	247	9 HUMMDR1A24	M29445 Human P-gly
4	19.4	92.4	2726	6 I33621	I33621 Sequence 1
5	19.4	92.4	3843	6 BD171402	BD171402 Method fo
6	19.4	92.4	3852	9 AF537133	AF537133 Macaca mu
7	19.4	92.4	3852	9 AF537134	AF537134 Macaca fa
8	19.4	92.4	3852	9 AY582534	AY582534 Macaca mu
9	19.4	92.4	3860	6 AX322787	AX322787 Sequence
10	19.4	92.4	3860	6 AX322789	AX322789 Sequence

11	19.4	92.4	4186	6	AR399194	AR399194 Sequence
12	19.4	92.4	4186	6	AX108654	AX108654 Sequence
13	19.4	92.4	4195	6	AR399195	AR399195 Sequence
14	19.4	92.4	4195	6	AX108656	AX108656 Sequence
15	19.4	92.4	4646	6	BD234195	BD234195 ATP-bindi
16	19.4	92.4	4646	6	I49610	I49610 Sequence 2
17	19.4	92.4	4646	6	AR380622	AR380622 Sequence
18	19.4	92.4	4646	6	AX336420	AX336420 Sequence
19	19.4	92.4	4646	6	AX336708	AX336708 Sequence
20	19.4	92.4	4646	6	AX391099	AX391099 Sequence
21	19.4	92.4	4646	6	AX504298	AX504298 Sequence
22	19.4	92.4	4646	9	HUMMDR1	M14758 Homo sapien
23	19.4	92.4	4669	6	AR055785	AR055785 Sequence
24	19.4	92.4	4669	6	AR091275	AR091275 Sequence
25	19.4	92.4	4669	6	I08557	I08557 Sequence 3
26	19.4	92.4	4669	6	AR203322	AR203322 Sequence
27	19.4	92.4	4669	6	AR363344	AR363344 Sequence
28	19.4	92.4	4669	6	AR405961	AR405961 Sequence
29	19.4	92.4	6505	6	AR028671	AR028671 Sequence
30	19.4	92.4	8630	6	AR306491	AR306491 Sequence
31	19.4	92.4	8630	6	AR306492	AR306492 Sequence
32	19.4	92.4	8630	6	AX012320	AX012320 Sequence
33	19.4	92.4	8630	6	AX012321	AX012321 Sequence
34	19.4	92.4	9318	6	AR028672	AR028672 Sequence
35	18.4	87.6	49	6	CQ815439	CQ815439 Sequence
C 36	18.4	87.6	207	6	CQ110395	CQ110395 Sequence
C 37	18.4	87.6	207	6	CQ149120	CQ149120 Sequence
C 38	18.4	87.6	207	6	CQ232394	CQ232394 Sequence
C 39	18.4	87.6	207	6	CQ270461	CQ270461 Sequence
C 40	18.4	87.6	207	6	CQ307708	CQ307708 Sequence
C 41	18.4	87.6	207	6	CQ344554	CQ344554 Sequence
C 42	18.4	87.6	472	6	CQ097213	CQ097213 Sequence
C 43	18.4	87.6	472	6	CQ136039	CQ136039 Sequence
C 44	18.4	87.6	472	6	CQ219337	CQ219337 Sequence
C 45	18.4	87.6	472	6	CQ257845	CQ257845 Sequence

Search completed: November 30, 2004, 17:04:43  
Job time : 731.333 secs

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:14 ; Search time 184 Seconds  
(without alignments)  
599.119 Million cell updates/sec

Title: SEQ1  
Perfect score: 21  
Sequence: 1 gtggtgtcacaggaagaggc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
1	19.4	92.4	247	8	ACF62747		Acf62747 Cancer ba
2	19.4	92.4	247	8	ADB20862		Adb20862 MRP1 base
3	19.4	92.4	247	10	ADB87951		Adb87951 Human UGT

4	19.4	92.4	247	10	ADB96934	Adb96934 Human MDR	
5	19.4	92.4	247	10	ADB92125	Adb92125 Human MDR	
6	19.4	92.4	247	12	ADK67453	Adk67453 Human MDR	
7	19.4	92.4	2726	2	AAQ70907	Aaq70907 Multidrug	
8	19.4	92.4	2726	2	AAQ70916	Aaq70916 Multidrug	
9	19.4	92.4	2726	2	AAT43322	Aat43322 Multidrug	
10	19.4	92.4	3843	6	ABQ78185	Abq78185 Human MDR	
11	19.4	92.4	3852	8	ABT14496	Abt14496 Rhesus mo	
12	19.4	92.4	3860	3	AAZ49332	Aaz49332 Human wil	
13	19.4	92.4	3860	3	AAZ49333	Aaz49333 Human G18	
14	19.4	92.4	3860	6	ABA94365	Aba94365 Human BCR	
15	19.4	92.4	3860	6	ABA94366	Aba94366 Human BCR	
16	19.4	92.4	4186	4	AAF86127	Aaf86127 Cynomolog	
17	19.4	92.4	4195	4	AAF86128	Aaf86128 Cynomolog	
18	19.4	92.4	4349	4	AAH57442	Aah57442 Human int	
19	19.4	92.4	4533	6	ABS65229	Abs65229 cDNA enco	
20	19.4	92.4	4646	2	AAQ72872	Aaq72872 Human mul	
21	19.4	92.4	4646	3	AAZ94738	Aaz94738 Human ATP	
22	19.4	92.4	4646	6	ABL68592	Ab168592 Kidney ca	
23	19.4	92.4	4646	6	ABL68880	Ab168880 Kidney ca	
24	19.4	92.4	4646	6	AAD38994	Aad38994 Human mdr	
25	19.4	92.4	4646	10	ADK60994	Adk60994 Ovarian c	
26	19.4	92.4	4646	11	ADI31841	Adi31841 Human cDN	
27	19.4	92.4	4669	1	AAN70752	Aan70752 Sequence	
28	19.4	92.4	4669	2	AAQ52726	Aaq52726 Sequence	
29	19.4	92.4	4669	2	AAV32645	Aav32645 Human P g	
30	19.4	92.4	4669	6	ABK52041	Abk52041 cDNA enco	
31	19.4	92.4	6505	2	AAT13394	Aat13394 Hybrid ve	
32	19.4	92.4	8630	3	AAZ24042	Aaz24042 Retrovira	
33	19.4	92.4	8630	3	AAZ24041	Aaz24041 Retrovira	
34	19	90.5	25	4	AAH21333	Aah21333 Human MDR	
35	18.4	87.6	31	4	AAI29774	Aai29774 Human sin	
36	18.4	87.6	49	12	ADP18688	Adp18688 Human MDR	
C	37	18.4	87.6	207	4	ABA70417	Aba70417 Human foe
C	38	18.4	87.6	207	4	AAI50568	Aai50568 Probe #19
C	39	18.4	87.6	207	4	AAK44585	Aak44585 Human bon
C	40	18.4	87.6	207	4	AAK18657	Aak18657 Human bra
C	41	18.4	87.6	207	4	ABS44243	Abs44243 Human liv
C	42	18.4	87.6	207	6	ABS18822	Abs18822 Human gen
C	43	18.4	87.6	430	10	ADC26767	Adc26767 Human lip
C	44	18.4	87.6	472	4	ABA57801	Aba57801 Human foe
C	45	18.4	87.6	472	4	AAI37386	Aai37386 Probe #60

Search completed: November 30, 2004, 17:16:16  
Job time : 187 secs

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:13 ; Search time 42.3333 Seconds  
(without alignments)  
352.596 Million cell updates/sec

Title: SEQ1  
Perfect score: 21  
Sequence: 1 gtggtgtcacaggaagggc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	SUMMARIES				
		Query		Description		
		Match	Length	DB	ID	
1	19.4	92.4	2726	1	US-08-461-823-1	Sequence 1, Appli
2	19.4	92.4	4186	4	US-09-672-810-1	Sequence 1, Appli
3	19.4	92.4	4195	4	US-09-672-810-3	Sequence 3, Appli
4	19.4	92.4	4646	1	US-08-181-471-2	Sequence 2, Appli
5	19.4	92.4	4646	4	US-09-023-655-1167	Sequence 1167, Ap
6	19.4	92.4	4669	2	US-08-583-276-18	Sequence 18, Appli
7	19.4	92.4	4669	2	US-08-752-447-1	Sequence 1, Appli
8	19.4	92.4	4669	3	US-09-316-167-1	Sequence 1, Appli
9	19.4	92.4	4669	4	US-09-397-233-1	Sequence 1, Appli

10	19.4	92.4	4669	6	5206352-3	Patent No. 5206352
11	19.4	92.4	6505	2	US-08-793-610-5	Sequence 5, Appli
12	19.4	92.4	8630	4	US-09-306-417-1	Sequence 1, Appli
13	19.4	92.4	8630	4	US-09-306-417-2	Sequence 2, Appli
14	19.4	92.4	9318	2	US-08-793-610-6	Sequence 6, Appli
15	18.4	87.6	3988	4	US-09-762-195-1	Sequence 1, Appli
16	18.4	87.6	4264	2	US-08-784-649A-1	Sequence 1, Appli
17	18.4	87.6	4264	2	US-08-784-649A-5	Sequence 5, Appli
18	16.8	80.0	315	4	US-09-248-796A-7498	Sequence 7498, Ap
C 19	16.8	80.0	229354	4	US-09-765-400-64	Sequence 64, Appl
C 20	16.8	80.0	229354	4	US-09-705-400-64	Sequence 64, Appl
C 21	16.4	78.1	512	4	US-09-495-050A-196	Sequence 196, App
C 22	16.4	78.1	517	3	US-09-276-531-13	Sequence 13, Appl
C 23	16.2	77.1	749	4	US-09-669-751-26	Sequence 26, Appl
C 24	16.2	77.1	767	4	US-09-220-132-13	Sequence 13, Appl
25	16.2	77.1	846	4	US-09-248-796A-3411	Sequence 3411, Ap
C 26	16.2	77.1	3090	5	PCT-US93-06251-7	Sequence 7, Appli
C 27	16.2	77.1	70000	4	US-09-851-896-3	Sequence 3, Appli
28	15.8	75.2	155	3	US-08-905-223-38	Sequence 38, Appl
29	15.8	75.2	613	4	US-09-270-767-15206	Sequence 15206, A
30	15.8	75.2	729	3	US-08-977-865-3	Sequence 3, Appli
C 31	15.8	75.2	1120	4	US-09-780-175-10	Sequence 10, Appl
32	15.8	75.2	1180	3	US-08-977-865-1	Sequence 1, Appli
33	15.8	75.2	1482	3	US-09-032-365A-16	Sequence 16, Appl
34	15.8	75.2	1525	3	US-08-812-824-2	Sequence 2, Appli
35	15.8	75.2	2331	4	US-09-866-028-54	Sequence 54, Appl
36	15.8	75.2	2331	4	US-09-944-457-54	Sequence 54, Appl
C 37	15.8	75.2	2439	3	US-08-969-317-1	Sequence 1, Appli
38	15.8	75.2	3352	3	US-09-231-227-3	Sequence 3, Appli
39	15.8	75.2	3352	4	US-09-768-585-3	Sequence 3, Appli
40	15.8	75.2	3636	3	US-09-074-579-2	Sequence 2, Appli
41	15.8	75.2	3636	3	US-09-388-774-2	Sequence 2, Appli
C 42	15.8	75.2	7874	4	US-09-780-175-96	Sequence 96, Appl
C 43	15.8	75.2	10807	1	US-08-206-176-7	Sequence 7, Appli
C 44	15.8	75.2	10807	2	US-08-756-506-5	Sequence 5, Appli
C 45	15.4	73.3	496	4	US-09-621-976-10729	Sequence 10729, A

GenCore version 5.1.6

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:09 ; Search time 727.333 Seconds  
(without alignments)  
1365.376 Million cell updates/sec

Title: SEQ3

Perfect score: 21

Sequence: 1 actataggccagagaggctgc 21

Scoring table: IDENTITY\_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:\*

1: gb\_ba:\*

2: gb\_htg:\*

3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
	No.	Score	Match	Length	DB	
-----	-----	-----	-----	-----	-----	-----
1	21	100.0	472	6	CQ097213	CQ097213 Sequence
2	21	100.0	472	6	CQ136039	CQ136039 Sequence
3	21	100.0	472	6	CQ219337	CQ219337 Sequence
4	21	100.0	472	6	CQ257845	CQ257845 Sequence

5	21	100.0	472	6	CQ295144	CQ295144 Sequence
6	21	100.0	472	6	CQ331767	CQ331767 Sequence
7	21	100.0	1022	6	AX597863	AX597863 Sequence
8	21	100.0	88483	2	AC079591	AC079591 Homo sapi
9	21	100.0	98472	6	AX706975	AX706975 Sequence
10	21	100.0	98472	6	AX707905	AX707905 Sequence
11	21	100.0	98472	9	AC005068	AC005068 Homo sapi
12	21	100.0	128993	6	AX706983	AX706983 Sequence
13	21	100.0	128993	6	AX707913	AX707913 Sequence
c 14	20.6	98.1	41	6	AX515221	AX515221 Sequence
c 15	20.6	98.1	41	6	AX517689	AX517689 Sequence
16	19.4	92.4	147436	2	AC079303	AC079303 Homo sapi
c 17	19.4	92.4	221722	2	AC130567	AC130567 Rattus no
18	19.4	92.4	235791	2	AC127050	AC127050 Rattus no
19	19	90.5	110000	2	AC074222_1	Continuation (2 of
c 20	19	90.5	138490	10	MMU249895	AJ249895 Mus muscu
21	19	90.5	203077	10	AC127172	AC127172 Mus muscu
c 22	19	90.5	203949	10	AL589878	AL589878 Mouse DNA
c 23	18.4	87.6	4329	6	CQ575681	CQ575681 Sequence
24	18.4	87.6	4671	3	BT009980	BT009980 Drosophil
25	18.4	87.6	4896	3	AY260051	AY260051 Drosophil
26	18.4	87.6	5255	3	AY568382	AY568382 Drosophil
27	18.4	87.6	5256	3	AY568384	AY568384 Drosophil
28	18.4	87.6	5256	3	AY568385	AY568385 Drosophil
29	18.4	87.6	5256	3	AY568386	AY568386 Drosophil
30	18.4	87.6	5257	3	AY568387	AY568387 Drosophil
31	18.4	87.6	5257	3	AY568388	AY568388 Drosophil
32	18.4	87.6	5258	3	AY568381	AY568381 Drosophil
33	18.4	87.6	5259	3	AY568389	AY568389 Drosophil
34	18.4	87.6	5260	3	AY568380	AY568380 Drosophil
35	18.4	87.6	5260	3	AY568383	AY568383 Drosophil
c 36	18.4	87.6	6007	6	CQ573833	CQ573833 Sequence
37	18.4	87.6	9985	3	AY260056	AY260056 Drosophil
38	18.4	87.6	9986	3	AY260057	AY260057 Drosophil
39	18.4	87.6	10645	3	AY260055	AY260055 Drosophil
c 40	18.4	87.6	32682	2	AC014984	AC014984 Drosophil
c 41	18.4	87.6	110000	2	AC102983_1	Continuation (2 of
c 42	18.4	87.6	150998	2	AC121511	AC121511 Mus muscu
43	18.4	87.6	163710	3	AC023709	AC023709 Drosophil
44	18.4	87.6	179363	3	AC023723	AC023723 Drosophil
c 45	18.4	87.6	197910	2	AC132287	AC132287 Mus muscu

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:14 ; Search time 184 Seconds  
(without alignments)  
599.119 Million cell updates/sec

Title: SEQ3  
Perfect score: 21  
Sequence: 1 actataggccagagaggctgc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query				Description
		Match	Length	DB	ID	
1	21	100.0	472	4	ABA57801	Aba57801 Human foe
2	21	100.0	472	4	AAI37386	Aai37386 Probe #60
3	21	100.0	472	4	AAK31504	Aak31504 Human bon
4	21	100.0	472	4	AAK05870	Aak05870 Human bra
5	21	100.0	472	4	ABS31186	Abs31186 Human liv
6	21	100.0	472	6	ABS06258	Abs06258 Human gen

C	7	21	100.0	98472	6	ABS54549	Abs54549 Human mul
	8	21	100.0	98472	8	ACF62745	Acf62745 Cancer ba
	9	21	100.0	98472	8	ADB20860	Adb20860 MRP1 base
	10	21	100.0	98472	10	ADB87949	Adb87949 Human UGT
	11	21	100.0	98472	10	ADB96932	Adb96932 Human MDR
	12	21	100.0	98472	10	ADB92123	Adb92123 Human MDR
	13	21	100.0	128993	8	ACF62749	Acf62749 Cancer ba
	14	21	100.0	128993	8	ADB20868	Adb20868 MRP1 base
	15	21	100.0	128993	10	ADB87957	Adb87957 Human UGT
	16	21	100.0	128993	10	ADB96940	Adb96940 Human MDR
	17	21	100.0	128993	10	ADB92131	Adb92131 Human MDR
C	18	20.6	98.1	430	10	ADC26767	Adc26767 Human lip
C	19	20	95.2	41	6	ABZ47103	Abz47103 Human ATP
C	20	20	95.2	41	6	ABZ44635	Abz44635 Human ATP
C	21	18.4	87.6	4329	4	ABL04132	Abl04132 Drosophil
C	22	18.4	87.6	6007	4	ABL02900	Abl02900 Drosophil
	23	17.8	84.8	1590	2	AAX76838	Aax76838 T66Bk-2 g
	24	17.8	84.8	2001	2	AAX76847	Aax76847 pCR.C3H-6
	25	17.8	84.8	2076	2	AAX76836	Aax76836 pCRth2-16
	26	17.8	84.8	2257	2	AAX76839	Aax76839 T66k-8 ge
	27	17.8	84.8	2827	2	AAX76837	Aax76837 T66Bk gen
	28	17.8	84.8	2827	2	AAX76878	Aax76878 pSV-T66Bk
	29	17.8	84.8	38186	2	AAZ32028	Aaz32028 Human MET
	30	17.8	84.8	38186	5	AAC90085	Aac90085 AC004449
C	31	17.4	82.9	6014	12	ADL35449	Adl35449 Human chr
C	32	16.8	80.0	44	4	AAF85562	Aaf85562 HIV TAR r
	33	16.8	80.0	7612	4	AAS36723	Aas36723 Human car
	34	16.8	80.0	7612	10	ADE47417	Ade47417 Human car
	35	16.4	78.1	493	4	ABA75418	Aba75418 Human foe
	36	16.4	78.1	493	4	AAK50048	Aak50048 Human bon
	37	16.4	78.1	493	4	AAK23982	Aak23982 Human bra
	38	16.4	78.1	493	6	ABS23534	Abs23534 Human gen
	39	16.4	78.1	599	4	ABA62915	Aba62915 Human foe
	40	16.4	78.1	599	4	AAK37112	Aak37112 Human bon
	41	16.4	78.1	599	4	AAK11323	Aak11323 Human bra
	42	16.4	78.1	599	6	ABS11110	Abs11110 Human gen
C	43	16.4	78.1	973	6	AAD42750	Aad42750 Rice GGPP
C	44	16.4	78.1	973	6	AAD42749	Aad42749 Rice GGPP
C	45	16.4	78.1	973	9	ACA05146	Aca05146 Rice gera

OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:13 ; Search time 42.3333 Seconds  
(without alignments)  
352.596 Million cell updates/sec

Title: SEQ3  
Perfect score: 21  
Sequence: 1 actataggccagagaggctgc 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:  
1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description
No.	Score	Match	Length	DB	ID	
<hr/>						
1	18.4	87.6	511	4	US-09-270-767-6977	Sequence 6977, Ap
2	18.4	87.6	511	4	US-09-270-767-22259	Sequence 22259, A
3	17.8	84.8	1590	4	US-09-554-726A-4	Sequence 4, Appli
4	17.8	84.8	2001	4	US-09-554-726A-15	Sequence 15, Appl
5	17.8	84.8	2076	4	US-09-554-726A-1	Sequence 1, Appli
6	17.8	84.8	2257	4	US-09-554-726A-6	Sequence 6, Appli
7	17.8	84.8	2827	4	US-09-554-726A-11	Sequence 11, Appl
8	17.8	84.8	2827	4	US-09-554-726A-20	Sequence 20, Appl
c 9	16.8	80.0	44	4	US-09-679-451-4	Sequence 4, Appli
c 10	16.2	77.1	800	4	US-09-221-017B-676	Sequence 676, App
11	16.2	77.1	1591	4	US-09-554-726A-17	Sequence 17, Appl
12	15.8	75.2	1326	4	US-09-489-039A-2375	Sequence 2375, Ap
c 13	15.8	75.2	3674	4	US-09-482-273-73	Sequence 73, Appl
c 14	15.8	75.2	6005	4	US-09-023-655-341	Sequence 341, App
15	15.8	75.2	12597	4	US-09-705-299-12	Sequence 12, Appl
16	15.8	75.2	1230025	4	US-09-198-452A-1	Sequence 1, Appli

c	17	15.4	73.3	287	4	US-09-313-294A-5604	Sequence 5604, Ap
	18	15.2	72.4	184	4	US-09-513-999C-26570	Sequence 26570, A
c	19	15.2	72.4	320	2	US-08-951-718-1	Sequence 1, Appli
	20	15.2	72.4	734	1	US-08-554-612C-21	Sequence 21, Appl
	21	15.2	72.4	836	1	US-08-554-612C-26	Sequence 26, Appl
	22	15.2	72.4	932	1	US-08-554-612C-20	Sequence 20, Appl
c	23	15.2	72.4	942	4	US-09-583-110-1575	Sequence 1575, Ap
	24	15.2	72.4	1007	1	US-08-554-612C-17	Sequence 17, Appl
	25	15.2	72.4	1007	1	US-08-554-612C-18	Sequence 18, Appl
	26	15.2	72.4	1308	2	US-08-404-531B-1	Sequence 1, Appli
	27	15.2	72.4	1308	2	US-08-404-531B-2	Sequence 2, Appli
	28	15.2	72.4	1308	3	US-08-476-900A-1	Sequence 1, Appli
	29	15.2	72.4	1308	3	US-08-476-900A-2	Sequence 2, Appli
	30	15.2	72.4	1308	3	US-08-488-546A-1	Sequence 1, Appli
	31	15.2	72.4	1308	3	US-08-488-546A-2	Sequence 2, Appli
	32	15.2	72.4	1508	1	US-08-554-612C-16	Sequence 16, Appl
	33	15.2	72.4	2229	4	US-09-454-495-1	Sequence 1, Appli
	34	15.2	72.4	2454	2	US-08-404-531B-32	Sequence 32, Appl
	35	15.2	72.4	2454	3	US-08-476-900A-32	Sequence 32, Appl
	36	15.2	72.4	2454	3	US-08-488-546A-32	Sequence 32, Appl
	37	15.2	72.4	2636	1	US-08-554-612C-12	Sequence 12, Appl
	38	15.2	72.4	2738	4	US-09-554-726A-9	Sequence 9, Appli
	39	15.2	72.4	2898	1	US-08-554-612C-51	Sequence 51, Appl
	40	15.2	72.4	2909	1	US-08-554-612C-10	Sequence 10, Appl
	41	15.2	72.4	2909	1	US-08-554-612C-11	Sequence 11, Appl
c	42	15.2	72.4	2938	3	US-09-072-917A-8	Sequence 8, Appli
	43	15.2	72.4	3729	1	US-08-554-612C-25	Sequence 25, Appl
	44	15.2	72.4	4931	3	US-08-726-320-2	Sequence 2, Appli
	45	15.2	72.4	4931	3	US-09-208-716-2	Sequence 2, Appli

Title: SEQ2  
 Perfect score: 21  
 Sequence: 1 gtgggtcacaggaagagg 21  
  
 Scoring table: IDENTITY\_NUC  
                   Gapop 10.0 , Gapext 1.0  
  
 Searched: 4526729 seqs, 23644849745 residues  
  
 Total number of hits satisfying chosen parameters: 9053458  
  
 Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000  
  
 Post-processing: Minimum Match 0%  
                   Maximum Match 100%  
                   Listing first 45 summaries  
  
 Database : GenEmbl:\*
   
 1: gb\_ba:\*
   
 2: gb\_htg:\*
   
 3: gb\_in:\*
   
 4: gb\_om:\*
   
 5: gb\_ov:\*
   
 6: gb\_pat:\*
   
 7: gb\_ph:\*
   
 8: gb\_pl:\*
   
 9: gb\_pr:\*
   
 10: gb\_ro:\*
   
 11: gb\_sts:\*
   
 12: gb\_sy:\*
   
 13: gb\_un:\*
   
 14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query					Description	
	No.	Score	Match	Length	DB	ID	
<hr/>							
c 1	1	19.4	92.4	49	6	CQ815439	CQ815439 Sequence
c 2	2	19.4	92.4	207	6	CQ110395	CQ110395 Sequence
c 3	3	19.4	92.4	207	6	CQ149120	CQ149120 Sequence
c 4	4	19.4	92.4	207	6	CQ232394	CQ232394 Sequence
c 5	5	19.4	92.4	207	6	CQ270461	CQ270461 Sequence
c 6	6	19.4	92.4	207	6	CQ307708	CQ307708 Sequence
c 7	7	19.4	92.4	207	6	CQ344554	CQ344554 Sequence
c 8	8	19.4	92.4	472	6	CQ097213	CQ097213 Sequence
c 9	9	19.4	92.4	472	6	CQ136039	CQ136039 Sequence
c 10	10	19.4	92.4	472	6	CQ219337	CQ219337 Sequence
c 11	11	19.4	92.4	472	6	CQ257845	CQ257845 Sequence
c 12	12	19.4	92.4	472	6	CQ295144	CQ295144 Sequence
c 13	13	19.4	92.4	472	6	CQ331767	CQ331767 Sequence

C	14	19.4	92.4	1022	6	AX597863	Sequence
	15	19.4	92.4	3840	6	AX481416	Sequence
	16	19.4	92.4	3988	6	BD190394	Phosphati
	17	19.4	92.4	3988	6	AR452556	Sequence
	18	19.4	92.4	3988	6	AX024454	Sequence
	19	19.4	92.4	4192	9	AF016535	Homo sapi
	20	19.4	92.4	4264	6	AR051647	Sequence
	21	19.4	92.4	4264	6	AR051650	Sequence
	22	19.4	92.4	4378	6	E02326	E02326 Multidrug r
	23	19.4	92.4	4553	6	CQ716151	CQ716151 Sequence
	24	19.4	92.4	4643	6	CQ815440	CQ815440 Sequence
	25	19.4	92.4	4643	6	AX522070	AX522070 Sequence
	26	19.4	92.4	4643	6	AX587788	AX587788 Sequence
C	27	19.4	92.4	88483	2	AC079591	AC079591 Homo sapi
C	28	19.4	92.4	98472	6	AX706975	AX706975 Sequence
C	29	19.4	92.4	98472	6	AX707905	AX707905 Sequence
C	30	19.4	92.4	98472	9	AC005068	AC005068 Homo sapi
C	31	19.4	92.4	128993	6	AX706983	AX706983 Sequence
C	32	19.4	92.4	128993	6	AX707913	AX707913 Sequence
C	33	19.4	92.4	147436	2	AC079303	AC079303 Homo sapi
	34	19	90.5	31	6	AX248183	AX248183 Sequence
	35	18.4	87.6	247	6	AX706977	AX706977 Sequence
	36	18.4	87.6	247	6	AX707907	AX707907 Sequence
	37	18.4	87.6	247	9	HUMMDR1A24	M29445 Human P-gly
C	38	18.4	87.6	1855	5	BC059436	BC059436 Danio rer
C	39	18.4	87.6	1881	5	BC065866	BC065866 Danio rer
	40	18.4	87.6	2726	6	I33621	I33621 Sequence 1
	41	18.4	87.6	3843	6	BD171402	BD171402 Method fo
	42	18.4	87.6	3852	9	AF537133	AF537133 Macaca mu
	43	18.4	87.6	3852	9	AF537134	AF537134 Macaca fa
	44	18.4	87.6	3852	9	AY582534	AY582534 Macaca mu
	45	18.4	87.6	3860	6	AX322787	AX322787 Sequence

Search completed: November 30, 2004, 17:04:45  
Job time : 729.333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:14 ; Search time 184 Seconds  
(without alignments)  
599.119 Million cell updates/sec

Title: SEQ2  
Perfect score: 21  
Sequence: 1 gtggtgtcacaggaagagg 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_23Sep04:\*

1: geneseqn1980s:\*

2: geneseqn1990s:\*

3: geneseqn2000s:\*

4: geneseqn2001as:\*

5: geneseqn2001bs:\*

6: geneseqn2002as:\*

7: geneseqn2002bs:\*

8: geneseqn2003as:\*

9: geneseqn2003bs:\*

10: geneseqn2003cs:\*

11: geneseqn2003ds:\*

12: geneseqn2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result	No.	Query					Description
		Score	Match	Length	DB	ID	
	1	19.4	92.4	31	4	AAI29774	Aai29774 Human sin
	2	19.4	92.4	49	12	ADP18688	Adp18688 Human MDR
C	3	19.4	92.4	207	4	ABA70417	Aba70417 Human foe

C	4	19.4	92.4	207	4	AAI50568	Aai50568 Probe #19
C	5	19.4	92.4	207	4	AAK44585	Aak44585 Human bon
C	6	19.4	92.4	207	4	AAK18657	Aak18657 Human bra
C	7	19.4	92.4	207	4	ABS44243	Abs44243 Human liv
C	8	19.4	92.4	207	6	ABS18822	Abs18822 Human gen
C	9	19.4	92.4	472	4	ABA57801	Aba57801 Human foe
C	10	19.4	92.4	472	4	AAI37386	Aai37386 Probe #60
C	11	19.4	92.4	472	4	AAK31504	Aak31504 Human bon
C	12	19.4	92.4	472	4	AAK05870	Aak05870 Human bra
C	13	19.4	92.4	472	4	ABS31186	Abs31186 Human liv
C	14	19.4	92.4	472	6	ABS06258	Abs06258 Human gen
	15	19.4	92.4	3840	6	ABV78146	Abv78146 Human mdr
	16	19.4	92.4	3840	6	ABZ35722	Abz35722 Human mdr
	17	19.4	92.4	3840	6	ABX09965	Abx09965 Human mdr
	18	19.4	92.4	3840	6	ABL91687	Ab191687 Human pol
	19	19.4	92.4	3988	3	AAZ88973	Aaz88973 Human MDR
	20	19.4	92.4	4264	2	AAV66533	Aav66533 Mutated h
	21	19.4	92.4	4264	2	AAV66534	Aav66534 Mutated h
	22	19.4	92.4	4378	2	AAQ04522	Aaq04522 Multidrug
	23	19.4	92.4	4643	6	ABS76368	Abs76368 cDNA enco
	24	19.4	92.4	4643	6	ABV94267	Abv94267 Breast ca
	25	19.4	92.4	4643	6	ABV74349	Abv74349 Human ABC
	26	19.4	92.4	4643	10	ABX77217	Abx77217 cDNA enco
	27	19.4	92.4	4643	12	ADP18689	Adp18689 Human MDR
	28	19.4	92.4	4643	12	ADO19748	Ado19748 Human PRO
	29	19.4	92.4	98472	6	ABS54549	Abs54549 Human mul
C	30	19.4	92.4	98472	8	ACF62745	Acf62745 Cancer ba
C	31	19.4	92.4	98472	8	ADB20860	Adb20860 MRP1 base
C	32	19.4	92.4	98472	10	ADB87949	Adb87949 Human UGT
C	33	19.4	92.4	98472	10	ADB96932	Adb96932 Human MDR
C	34	19.4	92.4	98472	10	ADB92123	Adb92123 Human MDR
C	35	19.4	92.4	128993	8	ACF62749	Acf62749 Cancer ba
C	36	19.4	92.4	128993	8	ADB20868	Adb20868 MRP1 base
C	37	19.4	92.4	128993	10	ADB87957	Adb87957 Human UGT
C	38	19.4	92.4	128993	10	ADB96940	Adb96940 Human MDR
C	39	19.4	92.4	128993	10	ADB92131	Adb92131 Human MDR
	40	19	90.5	25	4	AAH21333	Aah21333 Human MDR
	41	18.4	87.6	247	8	ACF62747	Acf62747 Cancer ba
	42	18.4	87.6	247	8	ADB20862	Adb20862 MRP1 base
	43	18.4	87.6	247	10	ADB87951	Adb87951 Human UGT
	44	18.4	87.6	247	10	ADB96934	Adb96934 Human MDR
	45	18.4	87.6	247	10	ADB92125	Adb92125 Human MDR

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OM nucleic - nucleic search, using sw model

Run on: November 30, 2004, 16:28:13 ; Search time 42.3333 Seconds  
(without alignments)  
352.596 Million cell updates/sec

Title: SEQ2  
Perfect score: 21  
Sequence: 1 gtgggtcacaggaagaggtt 21

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_NA:\*

1: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq:\*

2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*

3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*

4: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq:\*

5: /cgn2\_6/ptodata/1/ina/PCTUS\_COMB.seq:\*

6: /cgn2\_6/ptodata/1/ina/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	Query				Description	
No.	Score	Match	Length	DB	ID	
1	19.4	92.4	3988	4	US-09-762-195-1	Sequence 1, Appli
2	19.4	92.4	4264	2	US-08-784-649A-1	Sequence 1, Appli
3	19.4	92.4	4264	2	US-08-784-649A-5	Sequence 5, Appli
4	18.4	87.6	2726	1	US-08-461-823-1	Sequence 1, Appli
5	18.4	87.6	4186	4	US-09-672-810-1	Sequence 1, Appli
6	18.4	87.6	4195	4	US-09-672-810-3	Sequence 3, Appli
7	18.4	87.6	4646	1	US-08-181-471-2	Sequence 2, Appli
8	18.4	87.6	4646	4	US-09-023-655-1167	Sequence 1167, Ap
9	18.4	87.6	4669	2	US-08-583-276-18	Sequence 18, Appli
10	18.4	87.6	4669	2	US-08-752-447-1	Sequence 1, Appli
11	18.4	87.6	4669	3	US-09-316-167-1	Sequence 1, Appli

12	18.4	87.6	4669	4	US-09-397-233-1	Sequence 1, Appli
13	18.4	87.6	4669	6	5206352-3	Patent No. 5206352
14	18.4	87.6	6505	2	US-08-793-610-5	Sequence 5, Appli
15	18.4	87.6	8630	4	US-09-306-417-1	Sequence 1, Appli
16	18.4	87.6	8630	4	US-09-306-417-2	Sequence 2, Appli
17	18.4	87.6	9318	2	US-08-793-610-6	Sequence 6, Appli
18	17.8	84.8	315	4	US-09-248-796A-7498	Sequence 7498, Ap
c 19	16.4	78.1	512	4	US-09-495-050A-196	Sequence 196, App
c 20	16.4	78.1	517	3	US-09-276-531-13	Sequence 13, Appli
c 21	16.2	77.1	942	1	US-08-021-537-2	Sequence 2, Appli
22	15.8	75.2	155	3	US-08-905-223-38	Sequence 38, Appli
23	15.8	75.2	613	4	US-09-270-767-15206	Sequence 15206, A
c 24	15.8	75.2	1120	4	US-09-780-175-10	Sequence 10, Appli
c 25	15.8	75.2	2089	4	US-09-799-451-894	Sequence 894, App
26	15.8	75.2	2331	4	US-09-866-028-54	Sequence 54, Appli
27	15.8	75.2	2331	4	US-09-944-457-54	Sequence 54, Appli
28	15.8	75.2	3636	3	US-09-074-579-2	Sequence 2, Appli
29	15.8	75.2	3636	3	US-09-388-774-2	Sequence 2, Appli
c 30	15.8	75.2	7874	4	US-09-780-175-96	Sequence 96, Appli
c 31	15.8	75.2	10807	1	US-08-206-176-7	Sequence 7, Appli
c 32	15.8	75.2	10807	2	US-08-756-506-5	Sequence 5, Appli
c 33	15.8	75.2	229354	4	US-09-765-400-64	Sequence 64, Appli
c 34	15.8	75.2	229354	4	US-09-705-400-64	Sequence 64, Appli
35	15.8	75.2	786431	4	US-09-751-389-3	Sequence 3, Appli
c 36	15.4	73.3	290	4	US-09-513-999C-21911	Sequence 21911, A
c 37	15.4	73.3	496	4	US-09-621-976-10729	Sequence 10729, A
38	15.4	73.3	1668	4	US-09-614-221A-420	Sequence 420, App
39	15.4	73.3	10535	4	US-10-020-669-5	Sequence 5, Appli
40	15.2	72.4	228	4	US-09-248-796A-9476	Sequence 9476, Ap
41	15.2	72.4	513	4	US-09-248-796A-5545	Sequence 5545, Ap
c 42	15.2	72.4	749	4	US-09-669-751-26	Sequence 26, Appli
c 43	15.2	72.4	767	4	US-09-220-132-13	Sequence 13, Appli
44	15.2	72.4	846	4	US-09-248-796A-3411	Sequence 3411, Ap
45	15.2	72.4	1155	4	US-09-489-039A-6058	Sequence 6058, Ap